

Sequence Listing.ST25.txt
SEQUENCE LISTING

<110> Novo Nordisk Pharmaceuticals, Inc.
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Susanne, Bang
Olesen, Ole H
Petersen, Lars C

<120> Kunitz-Type Sequences and Polypeptides

<130> 6297.204-US

<140> To be assigned
<141> 2003-11-25

<150> Danish Application No. PA 2001 00859
<151> 2001-05-31

<150> US 60/303,180
<151> 2001-07-05

<150> PCT/DK02/00372
<151> 2002-05-31

<160> 34

<170> PatentIn version 3.2

<210> 1
<211> 58
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of human wild type HK1-18

<400> 1

Tyr Pro Val Arg Cys Leu Leu Pro Ser Ala His Gly Ser Cys Ala Asp
1 5 10 15

Trp Ala Ala Arg Trp Tyr Phe Val Ala Ser Val Gly Gln Cys Asn Arg
20 25 30

Phe Trp Tyr Gly Gly Cys His Gly Asn Ala Asn Asn Phe Ala Ser Glu
35 40 45

Gln Glu Cys Met Ser Ser Cys Gln Gly Ser
50 55

<210> 2
<211> 51
<212> PRT
<213> Artificial

<220>
<223> Synthetic

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<222> (2)..(2)
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      Arg, Phe, Tyr, Met, or is absent

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<222> (3)..(3)
<223> X in position 3 is Ala, Val, Leu, Ser, Thr, Asp, Glu, Gln, Phe,
      Met, or is absent

<220>
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<222> (4)..(4)
<223> X in position 4 is Gly, Ala, Leu, Ser, Asp, Lys, Glu, Gln, Pro,
      or is absent

<220>
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<222> (5)..(5)
<223> X in position 5 is Ala, Val, Leu, Glu, Ser, Asn, Lys, Glu, Tyr,
      Met, Pro, or is absent

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<222> (6)..(6)
<223> X in position 6 is Ala, Val, Leu, Ser, Asp, Asn, Lys, Glu, Arg,
      Tyr, Met, or is absent

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<222> (7)..(7)
<223> X in position 7 is Ala, Val, Thr, Asp, Lys, Glu, Gln, Arg, His,
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<222> (8)..(8)
<223> X in position 8 is Gly, Asp, or is absent

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<222> (9)..(9)
<223> X in position 9 is Leu, Glu, Ser, Thr, Asn, Gln, Arg, Pro, or is
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<222> (11)..(11)
<223> X in position 11 is Gly, Ala, Leu, Ser, Thr, Asn, Lys, Glu, Gln,
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<222> (12)..(12)
<223> X in position 12 is Gly, Ala, Thr, Asp, Glu, His, or is absent

<220>
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<222> (13)..(13)
<223> X in position 13 is Leu, Glu, Ser, Asn, Glu, Arg, Phe, Trp, Tyr,
      Met, or is absent

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<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> X in position 14 is Ala, Val, Leu, Glu, Thr, Glu, Phe, Met, or is
absent

<220>
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<222> (15)..(15)
<223> X in position 15 is Ala, Val, Leu, Glu, Ser, Thr, Asn, Lys, Glu,
Gln, Pro, or is absent

<220>
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<222> (16)..(16)
<223> X in position 16 is Leu, Lys, Arg, His, or is absent

<220>
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<222> (17)..(17)
<223> X in position 17 is Phe, Trp, Tyr, or is absent

<220>
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<222> (18)..(18)
<223> X in position 18 is Ala, His, Phe, Trp, Tyr, or is absent

<220>
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<222> (19)..(19)
<223> X in position 19 is Phe, Tyr, or is absent

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<221> MISC_FEATURE
<222> (20)..(20)
<223> X in position 20 is Val, Ser, Asp, Asn, Arg, or is absent

<220>
<221> MISC_FEATURE
<222> (21)..(21)
<223> X in position 21 is Gly, Ala, Leu, Glu, Ser, Asn, Lys, Phe, Pro,
or is absent

<220>
<221> MISC_FEATURE
<222> (22)..(22)
<223> X in position 22 is Val, Leu, Ser, Thr, Asn, Lys, Glu, Gln, Arg,
Phe, Tyr, or is absent

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<222> (23)..(23)
<223> X in position 23 is Ala, Val, Leu, Glu, Ser, Thr, Asp, Asn, Lys,
Glu, Arg, Tyr, or is absent

<220>
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<222> (24)..(24)
<223> X in position 24 is Gly, Asn, Lys, Glu, Gln, Arg, Tyr, Met, or is
absent

<220>

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<223> X in position 25 is Ala, Leu, Glu, Ser, Thr, Lys, Glu, Gln, Arg,
His, or is absent

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<222> (27)..(27)
<223> X in position 27 is Ala, Val, Ser, Thr, Asp, Asn, Lys, Glu, Gln,
Arg, His, or is absent

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<222> (28)..(28)
<223> X in position 28 is Ala, Leu, Ser, Thr, Asn, Lys, Glu, Gln, Arg,
Met, Pro, or is absent

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<222> (30)..(30)
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Pro, or is absent

<220>
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<222> (31)..(31)
<223> X in position 31 is Ser, Phe, Tyr, or is absent

<220>
<221> MISC_FEATURE
<222> (32)..(32)
<223> X in position 32 is Gly, Ser, Thr, Arg, or is absent

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<222> (35)..(35)
<223> X in position 35 is Gly, Leu, Asp, Asn, Glu, Gln, Arg, His, Tyr,
Met, or is absent

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<222> (36)..(36)
<223> X in position 36 is Gly, Ala, Arg, or is absent

<220>
<221> MISC_FEATURE
<222> (37)..(37)
<223> X in position 37 is Ser, Asp, Asn, Lys, or is absent

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<221> MISC_FEATURE
<222> (38)..(38)
<223> X in position 38 is Gly, Ala, Ser, Asp, Asn, Lys, Glu, Gln, Arg,
or is absent

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> X in position 40 is Ser, Asn, Lys, Arg, or is absent

<220>
<221> MISC_FEATURE
<222> (41)..(41)

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<223> X in position 41 is Phe, Tyr, or is absent

<220>
 <221> MISC_FEATURE
 <222> (42)..(42)
 <223> X in position 42 is Gly, Ala, Val, Leu, Thr, Asp, Asn, Lys, Glu, Gln, Arg, His, Tyr, Pro, or is absent

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 <222> (43)..(43)
 <223> X in position 43 is Ser, Thr, Asp, Asn, Glu, Arg, or is absent

<220>
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 <222> (44)..(44)
 <223> X in position 44 is Ala, Leu, Lys, Glu, Gln, Arg, Trp, or is absent

<220>
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 <222> (45)..(45)
 <223> X in position 45 is Ala, Asp, Lys, Glu, Gln, or is absent

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 <222> (46)..(46)
 <223> X in position 46 is Ala, Ser, Thr, Asp, Asn, Lys, Glu, Gln, Tyr, or is absent

<220>
 <221> MISC_FEATURE
 <222> (48)..(48)
 <223> X in position 48 is Leu, Ile, Glu, Asp, Lys, Glu, Gln, Arg, Met, or is absent

<220>
 <221> MISC_FEATURE
 <222> (49)..(49)
 <223> X in position 49 is Gly, Ala, Leu, Ser, Thr, Asp, Asn, Lys, Glu, Gln, Arg, or is absent

<220>
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 <222> (50)..(50)
 <223> X in position 50 is Ala, Ser, Thr, Val, Glu, Lys, Arg, Phe, Met, or is absent

<400> 2

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1				5					10					15	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Phe	Xaa	Xaa	Xaa
			20					25					30		

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Gly Cys Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
 35 40 45

Xaa Xaa Cys
 50

<210> 3
 <211> 174
 <212> DNA
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<400> 3
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 tggctacttcg ttgcctctgt gggccaatgt aaccgcttct ggtatggcgg ctgccatggc 120
 aatgccaata actttgcctc ggagcaagag tgcattgagca gctgccaggg atct 174

<210> 4
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 <213> Homo sapiens

<400> 4
 Tyr Pro Val Arg Cys Leu Leu Pro Pro Ala Thr Gly Pro Cys Lys Ala
 1 5 10 15

Arg Ile Ile Arg Trp Tyr Phe Val Ala Ser Val Gly Gln Cys Asn Arg
 20 25 30

Phe Val Tyr Gly Gly Cys Arg Gly Asn Ala Asn Asn Phe Ala Ser Glu
 35 40 45

Gln Glu Cys Met Ser Ser Cys Gln Gly Ser
 50 55

<210> 5
 <211> 58
 <212> PRT
 <213> Homo sapiens

<400> 5
 Tyr Pro Val Arg Cys Leu Leu Pro Pro Ala Thr Gly Pro Cys Arg Ala
 1 5 10 15

Arg Ile Ile Arg Trp Tyr Phe Val Ala Ser Val Gly Gln Cys Asn Arg
 20 25 30

Phe Val Tyr Gly Gly Cys Arg Gly Asn Ala Asn Asn Phe Ala Ser Glu
 35 40 45

Sequence Listing.ST25.txt

Gln Glu Cys Met Ser Ser Cys Gln Gly Ser
50 55

<210> 6
<211> 58
<212> PRT
<213> Homo sapiens

<400> 6

Tyr Pro Val Arg Cys Leu Leu Pro Pro Ala Thr Gly Ser Cys Lys Ala
1 5 10 15

Trp Ala Ala Arg Trp Tyr Phe Val Ala Ser Val Gly Gln Cys Asn Arg
20 25 30

Phe Trp Tyr Gly Gly Cys His Gly Asn Ala Asn Asn Phe Ala Ser Glu
35 40 45

Gln Glu Cys Met Ser Ser Cys Gln Gly Ser
50 55

<210> 7
<211> 58
<212> PRT
<213> Homo sapiens

<400> 7

Tyr Pro Val Arg Cys Leu Leu Pro Pro Ala Thr Gly Pro Cys Lys Ala
1 5 10 15

Arg Ala Ala Arg Trp Tyr Phe Val Ala Ser Val Gly Gln Cys Asn Arg
20 25 30

Phe Val Tyr Gly Gly Cys His Gly Asn Ala Asn Asn Phe Ala Ser Glu
35 40 45

Gln Glu Cys Met Ser Ser Cys Gln Gly Ser
50 55

<210> 8
<211> 18
<212> DNA
<213> Homo sapiens

<400> 8

acgccaagct ttggagcc

18

<210> 9
<211> 40
<212> DNA

Sequence Listing.ST25.txt

<213> Homo sapiens

<400> 9
ccttgatagg cccagccggc ctaccccgctg cggcgcctgc 40

<210> 10
<211> 39
<212> DNA
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<400> 10
ggatgtcaag cggccgcaga tccctggcag ctgctcatg 39

<210> 11
<211> 25
<212> DNA
<213> Homo sapiens

<400> 11
ctgcagaagc accatcaggt tgggtg 25

<210> 12
<211> 27
<212> DNA
<213> Homo sapiens

<400> 12
tctcttctcc aatctctcag ccatggc 27

<210> 13
<211> 47
<212> DNA
<213> Homo sapiens

<400> 13
catggctgag agattggaga agagataccc cgtgcggtgc ctgctgc 47

<210> 14
<211> 43
<212> DNA
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<400> 14
caggctgatc tagacttaag atccctggca gctgctcatg cac 43

<210> 15
<211> 25
<212> DNA
<213> Homo sapiens

<400> 15
caggaattcc attcaagaat agttc 25

<210> 16
<211> 30
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<213> Homo sapiens

<400> 16
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<211> 44
<212> DNA
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<400> 17
ctttggctaa cgtcgccatg gctgagagat tggagaagag atac 44

<210> 18
<211> 42
<212> DNA
<213> Homo sapiens

<400> 18
gggcagcagg caccgcacgg ggtatctctt ctccaatctc tc 42

<210> 19
<211> 42
<212> DNA
<213> Homo sapiens

<400> 19
ccgtgcggtg cctgctgccc cctgccactg gctcttgcaa ag 42

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<211> 44
<212> DNA
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<400> 20
gaagtaccag cgggcagccc aggctttgca agagccagtg gcag 44

<210> 21
<211> 44
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<213> Homo sapiens

<400> 21
gggctgcccg ctggtacttc gttgcctctg tgggccaatg taac 44

<210> 22
<211> 45
<212> DNA
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<400> 22
catgacagcc gccataccag aagcggttac attggcccac agagg 45

<210> 23
<211> 46
<212> DNA

Sequence Listing.ST25.txt

<213> Homo sapiens

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<210> 24
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<212> DNA
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<400> 24
cagctgctca tgcactcttg ctccgaggca aagttattgg 40

<210> 25
<211> 40
<212> DNA
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<210> 26
<211> 33
<212> DNA
<213> Homo sapiens

<400> 26
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<210> 27
<211> 42
<212> DNA
<213> Homo sapiens

<400> 27
ccgtgcggtg cctgctgccc cctgccactg gcccttgcaa ag 42

<210> 28
<211> 44
<212> DNA
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<400> 28
gaagtaccag cgggcagccc tggctttgca agggccagtg gcag 44

<210> 29
<211> 45
<212> DNA
<213> Homo sapiens

<400> 29
catgacagcc gccatacacg aagcgggttac attggcccac agagg 45

<210> 30
<211> 46
<212> DNA

Sequence Listing.ST25.txt

<213> Homo sapiens

<400> 30

cggtgatggc ggctgtcatg gcaatgccaa taactttgcc tcggag

46

<210> 31

<211> 419

<212> DNA

<213> Artificial

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<223> Nucleotide sequence encoding the 212L-HKI18 fusion polypeptide

<400> 31

gaattccatt caagaatagt tcaaacaaga agattacaaa ctatcaattt catacacaat 60

ataaacgacc aaaagaatga aggctgtttt cttggttttg tccttgatcg gattctgctg 120

ggcccaacca gtcactggcg atgaatcatc tgttgagatt ccggaagagt ctctgatcat 180

cgctgaaaac accacttttg ctaacgtcgc catggctgag agattggaga agagataccc 240

cgctgcggtgc ctgctgcca gtgccatgg ctcttgcgca gactgggctg cccgctggta 300

cttcgttgcc tctgtgggcc aatgtaaccg cttctggtat ggcggtgcc atggcaatgc 360

caataacttt gcctcggagc aagagtgcac gacgagctgc cagggatctt aagtctaga 419

<210> 32

<211> 111

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of the 212L-HKI18 fusion polypeptide

<400> 32

Met Lys Ala Val Phe Leu Val Leu Ser Leu Ile Gly Phe Cys Trp Ala
1 5 10 15

Gln Pro Val Thr Gly Asp Glu Ser Ser Val Glu Ile Pro Glu Glu Ser
20 25 30

Leu Ile Ile Ala Glu Asn Thr Thr Leu Ala Asn Val Ala Met Ala Glu
35 40 45

Arg Leu Glu Lys Arg Tyr Pro Val Arg Cys Leu Leu Pro Ser Ala His
50 55 60

Gly Ser Cys Ala Asp Trp Ala Ala Arg Trp Tyr Phe Val Ala Ser Val
65 70 75 80

Gly Gln Cys Asn Arg Phe Trp Tyr Gly Gly Cys His Gly Asn Ala Asn
85 90 95

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Asn Phe Ala Ser Glu Gln Glu Cys Met Ser Ser Cys Gln Gly Ser
100 105 110

<210> 33
<211> 111
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of the 212L-HKI18-1 fusion polypeptide
<400> 33

Met Lys Ala Val Phe Leu Val Leu Ser Leu Ile Gly Phe Cys Trp Ala
1 5 10 15

Gln Pro Val Thr Gly Asp Glu Ser Ser Val Glu Ile Pro Glu Glu Ser
20 25 30

Leu Ile Ile Ala Glu Asn Thr Thr Leu Ala Asn Val Ala Met Ala Glu
35 40 45

Arg Leu Glu Lys Arg Tyr Pro Val Arg Cys Leu Leu Pro Pro Ala Thr
50 55 60

Gly Ser Cys Lys Ala Trp Ala Ala Arg Trp Tyr Phe Val Ala Ser Val
65 70 75 80

Gly Gln Cys Asn Arg Phe Trp Tyr Gly Gly Cys His Gly Asn Ala Asn
85 90 95

Asn Phe Ala Ser Glu Gln Glu Cys Met Ser Ser Cys Gln Gly Ser
100 105 110

<210> 34
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<212> PRT
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<220>
<223> Amino acid sequence of the 212L-HKI18-2 fusion polypeptide
<400> 34

Met Lys Ala Val Phe Leu Val Leu Ser Leu Ile Gly Phe Cys Trp Ala
1 5 10 15

Gln Pro Val Thr Gly Asp Glu Ser Ser Val Glu Ile Pro Glu Glu Ser
20 25 30

Leu Ile Ile Ala Glu Asn Thr Thr Leu Ala Asn Val Ala Met Ala Glu
35 40 45

Sequence Listing.ST25.txt

Arg Leu Glu Lys Arg Tyr Pro Val Arg Cys Leu Leu Pro Pro Ala Thr
50 55 60

Gly Pro Cys Lys Ala Arg Ala Ala Arg Trp Tyr Phe Val Ala Ser Val
65 70 75 80

Gly Gln Cys Asn Arg Phe Val Tyr Gly Gly Cys His Gly Asn Ala Asn
85 90 95

Asn Phe Ala Ser Glu Gln Glu Cys Met Ser Ser Cys Gln Gly Ser
100 105 110